

97364

Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 6-24-2003
 Art Unit: _____ Phone Number 30 _____ Serial Number: 101032, 330
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL
CRI-11D13/CRI-9807

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Tissue Remodeling

Inventors (please provide full names): S. Ben-Sasson

Earliest Priority Filing Date: 12-31-2001

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID No: 21 (XGIVEEYQLPY) in STN,
 in the U.S. patent application sequence database (pending, published, & issued),
 and in Geneseq / Swissprot / PIR.

Thank you.

JER

STAFF USE ONLY

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel Orbit _____
Date Searcher Provided: _____	Bibliographic _____	Dr. Link _____
Date Completed: _____	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Client Prep Time: _____	Patent Family _____	WWW Internet _____
Other Time: _____	Other _____	Other (specify): _____

\$%^STN;HighlightOn= ***,HighlightOff=*** ;

=> d que l3

L1 70 SEA FILE=REGISTRY ABB=ON PLU=ON .GIVEEYQLPY/SQSP

L2 4 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<26

L3 3 SEA FILE=CAPLUS ABB=ON PLU=ON L2

=> d ibib abs hitstr 1-3

L3 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:850307 CAPLUS

DOCUMENT NUMBER: 137:346244

TITLE: Tissue remodeling with compds. comprising a sequence
from TGF-.beta. super family Ser/Thr/kinase receptors

INVENTOR(S): Ben-Sasson, Shmuel

PATENT ASSIGNEE(S): Children's Medical Center Corporation, USA

SOURCE: U.S. Pat. Appl. Publ., 51 pp., Cont.-in-part of Appl.
No. PCT/US00/32852.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2002165150	A1	20021107	US 2001-32330	20011231
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WO 2001042280	A2	20010614	WO 2000-US32852	20001204
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WO 2001042280	A3	20020307		
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1998-161094 B2 19980925

WO 2000-US32851 W 20001204

WO 2000-US32852 A2 20001204

US 1999-458491 A1 19991209

AB The invention concerns a method for the modulation of tissue-remodeling
processes, by contacting the tissue to be remodeled with a compd.
comprising a sequence derived from certain regions of TGF-.beta. super
family Ser/Thr/kinase receptors.

IT ***474526-96-0***

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)

(tissue remodeling with compds. comprising a sequence from TGF-.beta.

super family Ser/Thr/kinase receptors)
RN 474526-96-0 CAPLUS
CN L-Tyrosine, N-(1-oxotetradecyl)glycylglycyl-L-isoleucyl-L-valyl-L-.alpha.-
glutamyl-L-.alpha.-glutamyl-L-tyrosyl-L-glutamyl-L-leucyl-L-prolyl-
(9CI) (CA INDEX NAME)

Absolute stereochemistry.

/ Structure 1 in file .gra /

/ Structure 2 in file .gra /

L3 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:315483 CAPLUS

DOCUMENT NUMBER: 136:335268

TITLE: Short peptides which selectively modulate the activity
of serine/threonine kinases

INVENTOR(S): Ben-sasson, Shmuel A.

PATENT ASSIGNEE(S): The Children's Medical Center Corp., USA

SOURCE: U.S. Pat. Appl. Publ., 41 pp., Cont.-in-part of U. S.
6,174,993.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002049301	A1	20020425	US 2000-736076	20001213
US 6174993	B1	20010116	US 1997-861338	19970521
PRIORITY APPLN. INFO.:		US 1997-861338 A2 19970521		
OTHER SOURCE(S):		MARPAT 136:335268		

AB Peptides are disclosed which are peptide derivs. of the HJ loop of a serine/threonine kinase. The peptides can modulate the activity of the serine/threonine kinase. Also disclosed are methods of modulating the activity of a serine/threonine kinase in a subject by administering one of the peptides of the invention. The peptides can be used for the treatment of a wide variety of diseases.

IT ***415900-88-8*** ***415900-88-8D*** , derivs.

RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic

use); BIOL (Biological study); USES (Uses)
(peptide modulators of serine/threonine kinases)

RN 415900-88-8 CAPLUS

CN L-Tyrosinamide, N-(1-oxooctadecyl)glycylglycyl-L-isoleucyl-L-valyl-L-
.alpha.-glutamyl-L-.alpha.-glutamyl-L-tyrosyl-L-glutaminy-L-leucyl-L-
prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

/ Structure 3 in file .gra /

/ Structure 4 in file .gra /

RN 415900-88-8 CAPLUS

CN L-Tyrosinamide, N-(1-oxooctadecyl)glycylglycyl-L-isoleucyl-L-valyl-L-
.alpha.-glutamyl-L-.alpha.-glutamyl-L-tyrosyl-L-glutaminy-L-leucyl-L-
prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

/ Structure 5 in file .gra /

/ Structure 6 in file .gra /

IT ***416847-04-6***

RL: PRP (Properties)

(unclaimed sequence; short peptides which selectively modulate the
activity of serine/threonine kinases)

RN 416847-04-6 CAPLUS

CN L-Tyrosine, glycylglycyl-L-isoleucyl-L-valyl-L-.alpha.-glutamyl-L-.alpha.-
glutamyl-L-tyrosyl-L-glutaminy-L-leucyl-L-prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

/ Structure 7 in file .gra /

/ Structure 8 in file .gra /

L3 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:790656 CAPLUS

DOCUMENT NUMBER: 130:22236

TITLE: Short peptides which selectively modulate the activity
of serine/threonine kinases

INVENTOR(S): Ben-Sasson, Shmuel A.

PATENT ASSIGNEE(S): The Children's Medical Center Corp., USA; Yissum
Research Development Company of the Hebrew

SOURCE: PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 9853050	A2	19981126	WO 1998-US10319	19980520
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WO 9853050	A3	19990225		
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W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
CM, GA, GN, ML, MR, NE, SN, TD, TG

US 6174993	B1	20010116	US 1997-861338	19970521
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AU 9875833	A1	19981211	AU 1998-75833	19980520
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AU 734642	B2	20010621		
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EP 983346	A2	20000308	EP 1998-923571	19980520
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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO

JP 2002500649	T2	20020108	JP 1998-550580	19980520
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US 2002028772	A1	20020307	US 2000-735274	20001211
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US 2003004103	A1	20030102	US 2001-12035	20011211
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PRIORITY APPLN. INFO.: US 1997-861338 A2 19970521

WO 1998-US10319 W 19980520

US 2000-735274 A2 20001211

AB Disclosed are peptides which are peptide derivs. of the HJ loop of a
serine/threonine kinase. Modified peptides derivs. are provided from the
modified sequence or subsequence of the HJ loop of such kinases as RAF,

cAMP-dependent kinase, protein kinase C, the G protein-coupled receptor kinases .beta.ARK1, .beta.BARK2, GRK1 and GRKs4-6, calmodulin-dependent kinase, and Polo. The peptides can modulate the activity of the serine/threonine kinase. For example, peptide derivs. of the HJ loop of Raf and Polo inhibit the proliferation of bovine aortic cells and the transformed mouse cell lines MS1 and/or SVR cells in vitro at concns. as low as 10 .mu.M. Further examples include (1) inhibition of the prodn. of collagen by fetal lung fibroblasts by an HJ peptide deriv of activin/TGF.beta.R and (2) morphol. changes in B16 melanoma cells by an HJ peptide deriv. of integrin-linked kinase ILK. Also disclosed are methods of modulating the activity of a serine/threonine kinase in a subject by administering one of the peptides of the present invention.

IT ***216489-93-9***

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ALK3 kinase-derived; short peptides which selectively modulate the activity of serine/threonine kinases)

RN 216489-93-9 CAPLUS

CN L-Tyrosinamide, N-(1-oxotetradecyl)glycylglycyl-L-isoleucyl-L-valyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-tyrosyl-L-glutaminyl-L-leucyl-L-prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

/ Structure 9 in file .gra /

/ Structure 10 in file .gra /

OM protein - protein search, using sw model

Run on: June 25, 2003, 16:52:18 ; Search time 29 Seconds
(without alignments)
78.156 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length DB ID				Description
	Score						
1	54	98.2	286	6	Q8SPU4		Q8spu4 sus scrofa
2	54	98.2	371	6	Q8SPU3		Q8spu3 sus scrofa
3	54	98.2	493	4	Q8TBG2		Q8tbg2 homo sapien
4	54	98.2	500	11	Q60607		Q60607 mus musculu
5	54	98.2	502	6	Q9BDI4		Q9bdi4 ovis aries
6	54	98.2	502	6	Q95L23		Q95l23 sus scrofa
7	54	98.2	502	11	Q9QVT7		Q9qvt7 rattus sp.
8	54	98.2	502	13	Q9PUF4		Q9puf4 coturnix co
9	54	98.2	527	13	O42338		O42338 xenopus lae
10	54	98.2	527	13	O42339		O42339 xenopus lae
11	54	98.2	527	13	Q91578		Q91578 xenopus lae
12	54	98.2	530	13	Q9W629		Q9w629 brachydanio
13	54	98.2	532	11	Q64308		Q64308 rattus norv
14	54	98.2	533	13	Q9PUF5		Q9puf5 coturnix co
15	54	98.2	533	13	Q90754		Q90754 gallus gall
16	52	94.5	493	11	P70539		P70539 rattus norv
17	52	94.5	493	11	P70603		P70603 rattus norv
18	47	85.5	506	13	O73801		O73801 fugu rubrip
19	46	83.6	527	13	O93243		O93243 brachydanio
20	44	80.0	215	11	Q9CVP4		Q9cvp4 mus musculu
21	44	80.0	420	11	Q9D5H8		Q9d5h8 mus musculu
22	44	80.0	460	6	Q28531		Q28531 mustela sp.
23	44	80.0	499	6	O46680		O46680 bos taurus
24	44	80.0	500	13	Q91595		Q91595 xenopus lae
25	44	80.0	503	13	Q06900		Q06900 gallus gall
26	43	78.2	505	11	Q61271		Q61271 mus musculu
27	41	74.5	139	4	Q96QN2		Q96qn2 homo sapien
28	41	74.5	142	16	Q97NJ8		Q97nj8 streptococc
29	40	72.7	147	1	Q8X270		Q8x270 pyrococcus
30	40	72.7	505	13	P79689		P79689 brachydanio
31	40	72.7	601	5	Q23975		Q23975 drosophila
32	40	72.7	601	5	Q9V511		Q9v511 drosophila
33	40	72.7	694	11	Q8R099		Q8r099 mus musculu

34	39	70.9	498	13	Q91882	Q91882 xenopus lae
35	39	70.9	505	13	O57320	O57320 xenopus lae
36	39	70.9	506	13	O73736	O73736 brachydanio
37	39	70.9	506	13	Q9DGI6	Q9dgi6 brachydanio
38	39	70.9	507	13	O42475	O42475 xenopus lae
39	39	70.9	509	13	Q91432	Q91432 xenopus lae
40	39	70.9	535	5	Q95U21	Q95u21 drosophila
41	39	70.9	570	5	Q27931	Q27931 drosophila
42	39	70.9	694	11	Q8VBY4	Q8vby4 mus musculu
43	39	70.9	753	16	Q9KTK1	Q9ktk1 vibrio chol
44	39	70.9	948	3	O94603	O94603 schizosacch
45	38	69.1	167	4	Q96L27	Q96l27 homo sapien
46	38	69.1	167	11	O70549	O70549 mus musculu
47	38	69.1	562	16	Q99WW6	Q99ww6 staphylococ
48	38	69.1	1389	10	O24564	O24564 zea mays (m
49	37	67.3	345	5	Q8T930	Q8t930 tetrahymena
50	37	67.3	423	2	Q936A3	Q936a3 serratia ma
51	37	67.3	440	17	O58162	O58162 pyrococcus
52	37	67.3	780	5	O17471	O17471 schistosoma
53	37	67.3	1494	10	Q9M0E5	Q9m0e5 arabidopsis
54	36	65.5	42	8	Q8SMV5	Q8smv5 ilex fragil
55	36	65.5	95	15	O56072	O56072 human immun
56	36	65.5	201	6	Q8WNY4	Q8wny4 ovis aries
57	36	65.5	250	6	P79232	P79232 papio hamad
58	36	65.5	285	15	Q909K5	Q909k5 human immun
59	36	65.5	288	15	Q909K2	Q909k2 human immun
60	36	65.5	288	15	Q909K3	Q909k3 human immun
61	36	65.5	288	15	Q909K4	Q909k4 human immun
62	36	65.5	288	15	Q909K6	Q909k6 human immun
63	36	65.5	288	15	Q909K7	Q909k7 human immun
64	36	65.5	299	2	Q53744	Q53744 staphylococ
65	36	65.5	377	2	Q8RNP1	Q8rnp1 legionella
66	36	65.5	449	16	Q8RBL0	Q8rbl0 thermoanaer
67	36	65.5	502	11	Q91YV1	Q91yv1 mus musculu
68	36	65.5	502	11	Q91YR0	Q91yr0 mus musculu
69	36	65.5	504	11	Q63559	Q63559 rattus norv
70	36	65.5	504	13	Q9YH45	Q9yh45 gallus gall
71	36	65.5	504	13	Q90ZK6	Q90zk6 gallus gall
72	36	65.5	509	11	Q91VF1	Q91vf1 mus musculu
73	36	65.5	584	4	Q96DG3	Q96dg3 homo sapien
74	36	65.5	689	16	Q9KBA6	Q9kba6 bacillus ha
75	36	65.5	694	11	O70542	O70542 rattus norv
76	36	65.5	741	5	Q9UAG2	Q9uag2 ephydatia f
77	36	65.5	1005	10	Q9AYJ5	Q9ayj5 oryza sativ
78	36	65.5	1424	10	Q9FP69	Q9fp69 oryza sativ

79	36	65.5	1514	10	Q9LK64	Q9lk64 arabidopsis
80	36	65.5	1515	10	O24510	O24510 arabidopsis
81	35	63.6	81	2	Q9S5F2	Q9s5f2 escherichia
82	35	63.6	84	16	Q8XGQ3	Q8xgq3 salmonella
83	35	63.6	113	17	Q9UXD9	Q9uxd9 sulfolobus
84	35	63.6	163	5	Q9XXD4	Q9xxd4 caenorhabdi
85	35	63.6	175	6	Q9GLC1	Q9glc1 sus scrofa
86	35	63.6	208	5	Q95VX8	Q95vx8 trypanosoma
87	35	63.6	208	5	Q95VX7	Q95vx7 trypanosoma
88	35	63.6	208	5	Q95VX6	Q95vx6 trypanosoma
89	35	63.6	208	5	Q95NW3	Q95nw3 trypanosoma
90	35	63.6	216	5	Q9VJZ6	Q9vjb6 drosophila
91	35	63.6	224	2	Q9KI73	Q9ki73 shigella dy
92	35	63.6	225	2	Q9KI75	Q9ki75 erwinia chr
93	35	63.6	227	5	O44964	O44964 caenorhabdi
94	35	63.6	233	13	Q9PSG2	Q9psg2 gallus gall
95	35	63.6	245	16	Q8RHB9	Q8rhb9 fusobacteri
96	35	63.6	254	6	P79233	P79233 papio hamad
97	35	63.6	272	10	Q9FM27	Q9fm27 arabidopsis
98	35	63.6	280	16	Q99Q22	Q99q22 streptomyce
99	35	63.6	282	10	O65412	O65412 arabidopsis
100	35	63.6	292	13	Q9PSG1	Q9psg1 gallus gall

ALIGNMENTS

RESULT 1

Q8SPU4

ID Q8SPU4 PRELIMINARY; PRT; 286 AA.

AC Q8SPU4;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Bone morphogenic protein receptor type IB (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Kim J.G., Song J.H., Vallet J.L., Rohrer G.A., Christenson R.K.;

RT "Characterization of porcine bone morphogenic protein receptor-IB

RT (BMPR-IB).";

RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF488733; AAM00923.1; -.

KW Receptor.

FT NON_TER 1 1

SQ SEQUENCE 286 AA; 32800 MW; C1A9CC13F57ECBFE CRC64;

Query Match 98.2%; Score 54; DB 6; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

|||||||

Db 202 GIVEEYQLPY 211

Search completed: June 25, 2003, 16:59:40

Job time : 33 secs

OM protein - protein search, using sw model

Run on: June 25, 2003, 16:51:52 ; Search time 11 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB ID	Description
	Score	Match				
1	54	98.2	502	1	BMRB_CHICK	Q05438 gallus gall
2	54	98.2	502	1	BMRB_HUMAN	O00238 homo sapien
3	54	98.2	502	1	BMRB_MOUSE	P36898 mus musculu
4	54	98.2	532	1	BMRA_HUMAN	P36894 homo sapien
5	54	98.2	532	1	BMRA_MOUSE	P36895 mus musculu

6	46	83.6	505	1	KIR2_HUMAN	P36896 homo sapien
7	46	83.6	505	1	KIR2_RAT	P80202 rattus norv
8	44	80.0	501	1	TGR1_RAT	P80204 rattus norv
9	44	80.0	503	1	TGR1_HUMAN	P36897 homo sapien
10	44	80.0	503	1	TGR1_MOUSE	Q64729 mus musculu
11	42	76.4	695	1	CASP_MESAU	P15156 mesocricetu
12	41	74.5	688	1	C1S_HUMAN	P09871 homo sapien
13	38	69.1	167	1	TELT_HUMAN	O15273 homo sapien
14	38	69.1	167	1	TELT_MOUSE	O70548 mus musculu
15	36	65.5	299	1	VGB_STAAU	P17978 staphylococ
16	36	65.5	502	1	KIR3_MOUSE	Q61288 mus musculu
17	36	65.5	503	1	KIR3_HUMAN	P37023 homo sapien
18	36	65.5	505	1	KIR3_RAT	P80203 rattus norv
19	36	65.5	509	1	AVR1_BOVIN	Q28041 bos taurus
20	36	65.5	509	1	AVR1_HUMAN	Q04771 homo sapien
21	36	65.5	509	1	AVR1_MOUSE	P37172 mus musculu
22	36	65.5	509	1	AVR1_RAT	P80201 rattus norv
23	36	65.5	547	1	GSPA_AERHY	P45754 aeromonas h
24	36	65.5	584	1	LIGA_HUMAN	P41214 homo sapien
25	35	63.6	85	1	YNAJ_ECOLI	P76050 escherichia
26	35	63.6	251	1	REE1_ECOLI	P03856 escherichia
27	35	63.6	467	1	E2BD_SCHPO	Q09924 schizosacch
28	35	63.6	504	1	COA3_AAV2	P03135 adeno-assoc
29	35	63.6	512	1	AVRB_BOVIN	Q95126 bos taurus
30	35	63.6	512	1	AVRB_HUMAN	Q13705 homo sapien
31	35	63.6	513	1	AVR2_BOVIN	Q28043 bos taurus
32	35	63.6	513	1	AVR2_HUMAN	P27037 homo sapien
33	35	63.6	513	1	AVR2_MOUSE	P27038 mus musculu
34	35	63.6	513	1	AVR2_RAT	P38444 rattus norv
35	35	63.6	513	1	AVR2_SHEEP	Q28560 ovis aries
36	35	63.6	514	1	AVR2_XENLA	P27039 xenopus lae
37	35	63.6	536	1	AVRB_MOUSE	P27040 mus musculu
38	35	63.6	578	1	HPCL_HUMAN	Q9uj83 homo sapien
39	34	61.8	306	1	DDL_YERPE	Q8zie7 yersinia pe
40	34	61.8	321	1	EUM1_EURMA	P25780 euroglyphus
41	34	61.8	321	1	MMAL_DERFA	P16311 dermatophag
42	34	61.8	330	1	YC78_SYNY3	P74192 synechocyst
43	34	61.8	398	1	ENO_HALN1	Q9hqi9 halobacteri
44	34	61.8	428	1	SYS_CHLMU	Q9plj7 chlamydia m
45	34	61.8	469	1	TPS1_YARLI	O74932 yarrowia li
46	34	61.8	551	1	YVD3_CAEEL	P55114 caenorhabdi
47	34	61.8	715	1	KARG_ANTJA	O15992 anthopleura
48	34	61.8	836	1	PDC2_CANAL	O60035 candida alb
49	34	61.8	1333	1	CC25_CANAL	P43069 candida alb
50	34	61.8	1724	1	PPOV_HUMAN	Q9ukk3 homo sapien

51	33.5	60.9	895	1	YP67_CAEEL	Q09216 caenorhabdi
52	33	60.0	251	1	REE2_ECOLI	P33456 escherichia
53	33	60.0	305	1	YQBB_BACSU	P45918 bacillus su
54	33	60.0	319	1	YC39_ODOSI	P49534 odontella s
55	33	60.0	364	1	YD5A_METJA	P58018 methanococc
56	33	60.0	400	1	ENO_HALMA	P29201 haloarcula
57	33	60.0	424	1	SAHH_METKA	P58855 methanopyru
58	33	60.0	426	1	VP8_RGDV	P29077 rice gall d
59	33	60.0	507	1	VL1_HP37	P50813 human papil
60	33	60.0	511	1	AVRB_XENLA	P27041 xenopus lae
61	33	60.0	532	1	TYRO_RANNI	Q04604 rana nigrom
62	33	60.0	785	1	YHY2_YEAST	P38870 saccharomyc
63	33	60.0	993	1	EPA7_CHICK	O42422 gallus gall
64	33	60.0	998	1	EPA7_HUMAN	Q15375 homo sapien
65	33	60.0	998	1	EPA7_MOUSE	Q61772 mus musculu
66	33	60.0	998	1	EPA7_RAT	P54759 rattus norv
67	33	60.0	2052	1	UBRB_SCHPO	O13731 schizosacch
68	33	60.0	3135	1	S230_PLAFO	Q08372 plasmodium
69	32	58.2	215	1	KAD_LISIN	Q927m8 listeria in
70	32	58.2	215	1	KAD_LISMO	Q8y449 listeria mo
71	32	58.2	324	1	DDL_CAUCR	Q9a5a9 caulobacter
72	32	58.2	382	1	AVRB_RAT	P38445 rattus norv
73	32	58.2	395	1	Y414_METJA	Q57857 methanococc
74	32	58.2	428	1	SYS_CHLTR	O84734 chlamydia t
75	32	58.2	462	1	CATC_MOUSE	P97821 mus musculu
76	32	58.2	462	1	CATC_RAT	P80067 rattus norv
77	32	58.2	506	1	VL1_HP23	P50789 human papil
78	32	58.2	507	1	VL1_HP17	Q02514 human papil
79	32	58.2	510	1	VL1_HP22	P50788 human papil
80	32	58.2	510	1	VL1_HP38	P50814 human papil
81	32	58.2	667	1	EM70_YEAST	P32802 saccharomyc
82	32	58.2	692	1	VNUC_MABVM	P27588 marburg vir
83	32	58.2	695	1	VNUC_MABVP	P35263 marburg vir
84	32	58.2	806	1	SYL_HELPJ	Q9zj63 helicobacte
85	32	58.2	806	1	SYL_HELPY	P56457 helicobacte
86	32	58.2	877	1	EPA5_MOUSE	Q60629 mus musculu
87	32	58.2	930	1	DPO1_HAEIN	P43741 haemophilus
88	32	58.2	1002	1	EPB5_CHICK	Q07497 gallus gall
89	32	58.2	1002	1	POL_HV1EL	P04589 human immun
90	32	58.2	1002	1	POL_HV1ND	P18802 human immun
91	32	58.2	1002	1	POL_HV1RH	P05959 human immun
92	32	58.2	1002	1	POL_HV1Z2	P12499 human immun
93	32	58.2	1003	1	POL_HV1A2	P03369 human immun
94	32	58.2	1003	1	POL_HV1H2	P04585 human immun
95	32	58.2	1003	1	POL_HV1N5	P12497 human immun

96	32	58.2	1003	1	POL_HV10Y	P20892 human immun
97	32	58.2	1003	1	POL_HV1Y2	P35963 human immun
98	32	58.2	1004	1	EPA8_MOUSE	O09127 mus musculu
99	32	58.2	1005	1	EPA5_RAT	P54757 rattus norv
100	32	58.2	1005	1	EPA8_HUMAN	P29322 homo sapien

ALIGNMENTS

RESULT 1

BMRB_CHICK

ID BMRB_CHICK STANDARD; PRT; 502 AA.

AC Q05438;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein receptor type IB precursor (EC 2.7.1.37)

DE (Serine/threonine-protein kinase receptor R6) (SKR6) (Activin

DE receptor-like kinase 6) (ALK-6) (RPK-1).

GN BMPR1B.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94003400; PubMed=8400359;

RA Yamazaki Y., Saito T., Nohno T.;

RT "A new receptor protein kinase from chick embryo related to type II

RT receptor for TGF-beta.";

RL DNA Seq. 3:297-302(1993).

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SUBUNIT: HETERODIMERIZE WITH A TYPE-II RECEPTOR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC TGFB RECEPTOR SUBFAMILY.

CC -----

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 CC -----
 DR EMBL; D13432; BAA02694.1; -.
 DR HSSP; P36897; 1TBI.
 DR InterPro; IPR000472; Activin_rec.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR003605; TGFbeta_GS.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01064; Activin_recp; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00467; GS; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 13 POTENTIAL.
 FT CHAIN 14 502 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE
 FT IB.
 FT DOMAIN 14 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 148 POTENTIAL.
 FT DOMAIN 149 502 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 204 494 PROTEIN KINASE.
 FT NP_BIND 210 218 ATP (BY SIMILARITY).
 FT BINDING 231 231 ATP (BY SIMILARITY).
 FT ACT_SITE 332 332 BY SIMILARITY.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 502 AA; 56766 MW; D5D93CCEBF2A0680 CRC64;

Query Match 98.2%; Score 54; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11
 |||||
 Db 418 GIVEEYQLPY 427

RESULT 2
 BMRB_HUMAN
 ID BMRB_HUMAN STANDARD; PRT; 502 AA.
 AC O00238; P78366;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein receptor type IB precursor (EC 2.7.1.37).
 GN BMPR1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=97322244; PubMed=9178898;
 RA Ide H., Katoh M., Sasaki H., Yoshida T., Aoki K., Nawa Y., Osada Y.,
 RA Sugimura T., Terada M.;
 RT "Cloning of human bone morphogenetic protein type IB receptor (BMPR-
 RT IB) and its expression in prostate cancer in comparison with other
 RT BMPRs.";
 RL Oncogene 14:1377-1382(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Astrom A.-K., Jin D.F., Imamura T., Roijer E., Rosenzweig B.,
 RA Miyazono K., ten Dijke P., Stenman G.;
 RT "Chromosomal localization of three human genes encoding bone
 RT morphogenetic protein receptors.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR BMPS/OP-1.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: HETERODIMERIZE WITH A TYPE-II RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF β RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; D89675; BAA19765.1; -.
 DR EMBL; U89326; AAC28131.1; -.
 DR Genew; HGNC:1077; BMPR1B.
 DR MIM; 603248; -.
 DR InterPro; IPR000472; Activin_rec.

DR InterPro; IPR000333; Actn_receptorII.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR003605; TGFbeta_GS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01064; Activin_recp; 1.
 DR PRINTS; PR00653; ACTIVIN2R.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00467; GS; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Signal.
 FT SIGNAL 1 13 POTENTIAL.
 FT CHAIN 14 502 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE
 FT IB.
 FT DOMAIN 14 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 148 POTENTIAL.
 FT DOMAIN 149 502 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 204 494 PROTEIN KINASE.
 FT NP_BIND 210 218 ATP (BY SIMILARITY).
 FT BINDING 231 231 ATP (BY SIMILARITY).
 FT ACT_SITE 332 332 BY SIMILARITY.
 SQ SEQUENCE 502 AA; 56930 MW; B283D9BF45535C79 CRC64;

Query Match 98.2%; Score 54; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11
 |||||
 Db 418 GIVEEYQLPY 427

Search completed: June 25, 2003, 16:59:03
 Job time : 14 secs

OM protein - protein search, using sw model

Run on: June 25, 2003, 16:57:37 ; Search time 15 Seconds
(without alignments)
70.499 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description
1	54	98.2	502	2	A56683		receptor protein k

2	54	98.2	502	2	A53444	activin receptor-l
3	54	98.2	502	2	JC2491	serine/threonine k
4	54	98.2	527	2	A54985	BMP receptor precu
5	54	98.2	532	2	I37163	ALK-3 - human
6	54	98.2	532	2	A56238	bone morphogenetic
7	54	98.2	532	2	JC2387	bone morphogenetic
8	46	83.6	476	2	I80182	activin type I rec
9	46	83.6	505	2	I38859	activin A receptor
10	46	83.6	505	2	I53417	type I serine-thre
11	44	80.0	440	2	A56693	receptor protein k
12	44	80.0	499	2	JC2062	transforming growt
13	44	80.0	503	2	A49432	activin receptor-l
14	44	80.0	503	2	JC2061	transforming growt
15	42	76.4	695	1	S05008	complement subcomp
16	41	74.5	142	2	D95237	phosphotyrosine pr
17	41	74.5	688	1	C1HUS	complement subcomp
18	40	72.7	601	2	A55921	serine/threonine k
19	39	70.9	570	2	I45712	Dpp receptor SAX p
20	39	70.9	753	2	E82265	hypothetical prote
21	39	70.9	948	2	T41496	conserved hypothet
22	38	69.1	142	2	E98101	conserved hypothet
23	38	69.1	562	2	D89789	hypothetical prote
24	38	69.1	1389	2	T03273	embryogenesis tran
25	37	67.3	440	2	B71153	hypothetical prote
26	36	65.5	247	2	PC4260	activin type I rec
27	36	65.5	299	2	PN0638	vgh protein - Stap
28	36	65.5	389	2	T47178	hypothetical prote
29	36	65.5	502	2	JC4337	activin receptor l
30	36	65.5	502	2	I48241	ALK-1 - mouse
31	36	65.5	503	2	A49431	activin/TGF-beta-l
32	36	65.5	509	2	A45992	activin A receptor
33	36	65.5	509	2	I59576	transforming growt
34	36	65.5	509	2	A49664	activin type I rec
35	36	65.5	547	2	I39593	exeA protein - Aer
36	36	65.5	689	2	F83902	beta-galactosidase
37	36	65.5	694	2	JC6554	complement subcomp
38	36	65.5	1515	2	T52081	MRP-like ABC trans
39	35	63.6	81	2	T00242	rep protein - Esch
40	35	63.6	84	2	AC0662	probable membrane
41	35	63.6	85	2	A90868	hypothetical prote
42	35	63.6	85	2	H85750	hypothetical prote
43	35	63.6	85	2	G64882	membrane protein y
44	35	63.6	113	2	G90223	DNA-directed RNA p
45	35	63.6	163	2	T26980	hypothetical prote
46	35	63.6	227	2	T32894	hypothetical prote

47	35	63.6	251	1	QQECF	Replication initia
48	35	63.6	251	2	PC4261	activin type II re
49	35	63.6	282	2	T05155	hypothetical prote
50	35	63.6	382	2	B49193	type II activin re
51	35	63.6	408	2	C86903	hypothetical prote
52	35	63.6	453	2	D69828	conserved hypothet
53	35	63.6	457	2	T49169	hypothetical prote
54	35	63.6	467	2	S62591	translation initia
55	35	63.6	504	1	VCPV3A	coat protein - ade
56	35	63.6	504	2	B40829	activin receptor i
57	35	63.6	512	2	S21171	activin receptor S
58	35	63.6	512	2	D40829	activin receptor i
59	35	63.6	512	2	I37134	activin type II re
60	35	63.6	513	1	JQ1486	activin receptor I
61	35	63.6	513	2	S23089	activin receptor t
62	35	63.6	513	2	A39896	activin receptor p
63	35	63.6	513	2	A49193	type II activin re
64	35	63.6	513	2	S27258	activin receptor t
65	35	63.6	513	2	JQ1484	activin receptor p
66	35	63.6	513	2	I45850	activin receptor t
67	35	63.6	514	2	JQ1317	activin receptor p
68	35	63.6	528	2	C40829	activin receptor i
69	35	63.6	536	2	A40829	activin receptor i
70	35	63.6	540	2	T03309	gene 12 protein, p
71	35	63.6	571	2	A81797	hypothetical prote
72	35	63.6	611	2	C84863	hypothetical prote
73	35	63.6	1417	2	AG2137	hypothetical prote
74	35	63.6	1939	2	AF0095	probable sideropho
75	34	61.8	119	2	S23941	dipeptidyl-peptida
76	34	61.8	173	2	A72262	adenine phosphorib
77	34	61.8	211	2	S21864	probable cysteine
78	34	61.8	306	2	AB0069	D-alanine-D-alanin
79	34	61.8	319	2	A61500	allergen Der f I p
80	34	61.8	330	2	S75822	hypothetical prote
81	34	61.8	346	2	A96926	endoglucanase, ami
82	34	61.8	390	2	B82265	hypothetical prote
83	34	61.8	392	2	G83575	conserved hypothet
84	34	61.8	398	2	B84270	phosphopyruvate hy
85	34	61.8	398	2	S76445	hypothetical prote
86	34	61.8	428	2	C81742	seryl-tRNA synthet
87	34	61.8	551	2	T16557	hypothetical prote
88	34	61.8	610	2	A84417	hypothetical prote
89	34	61.8	1333	2	S30356	CDC25 protein homo
90	34	61.8	1691	1	D54689	protein-tyrosine-p
91	34	61.8	1894	2	C54689	protein-tyrosine-p

92	33.5	60.9	863	2	D88216	protein B0495.7 [i
93	33	60.0	144	2	D84287	hypothetical prote
94	33	60.0	238	2	G72311	conserved hypothet
95	33	60.0	251	1	QQECR7	gene E protein - E
96	33	60.0	251	2	C84036	succinate dehydrog
97	33	60.0	274	2	F81350	formyltetrahydrofo
98	33	60.0	282	2	D81326	5,10-methylenetet
99	33	60.0	287	2	T01192	hypothetical prote
100	33	60.0	305	2	E69946	hypothetical prote

ALIGNMENTS

RESULT 1

A56683

receptor protein kinase RPK-1 precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999

C;Accession: A56683

R;Sumitomo, S.; Saito, T.; Nohno, T.

DNA Seq. 3, 297-302, 1993

A;Title: A new receptor protein kinase from chick embryo related to type II receptor for TGF-beta.

A;Reference number: A56683; MUID:94003400; PMID:8400359

A;Accession: A56683

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-502 <SUM>

A;Cross-references: GB:D13432; NID:g222862; PIDN:BAA02694.1; PID:d1003199; PID:g222863

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C;Keywords: ATP; phosphotransferase; transmembrane protein

F;202-498/Domain: protein kinase homology <KIN>

F;210-218/Region: protein kinase ATP-binding motif

Query Match 98.2%; Score 54; DB 2; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

|||||||

Db 418 GIVEEYQLPY 427

RESULT 2

A53444

activin receptor-like kinase 6 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999

C;Accession: A53444; S40159

R;ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin, C.H.
Science 264, 101-104, 1994

A;Title: Characterization of type I receptors for transforming growth factor-beta and activin.

A;Reference number: A53444; MUID:94188705; PMID:8140412

A;Accession: A53444

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-502 <TEN>

A;Cross-references: GB:Z23143; NID:g437870; PIDN:CAA80674.1; PID:g437871

R;Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993

A;Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kinase
receptor family.

A;Reference number: S40158

A;Accession: S40159

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-502 <MIY>

A;Cross-references: EMBL:Z23143; NID:g437870; PIDN:CAA80674.1; PID:g437871

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C;Keywords: ATP; serine/threonine-specific protein kinase; transmembrane protein

F;202-498/Domain: protein kinase homology <KIN>

F;210-218/Region: protein kinase ATP-binding motif

Query Match 98.2%; Score 54; DB 2; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

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Db 418 GIVEEYQLPY 427

Search completed: June 25, 2003, 17:00:02

Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 16:59:48 ; Search time 19 Seconds
(without alignments)
62.646 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*

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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Score					
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2	54	98.2	11	9	US-10-032-330-22	Sequence 22, Appl
3	54	98.2	11	10	US-09-736-076-25	Sequence 25, Appl
4	54	98.2	11	10	US-09-736-076-67	Sequence 67, Appl
5	54	98.2	31	9	US-10-032-330-37	Sequence 37, Appl
6	54	98.2	493	9	US-09-069-228-2	Sequence 2, Appli
7	54	98.2	502	9	US-09-982-543A-8	Sequence 8, Appli
8	54	98.2	502	9	US-10-044-716-14	Sequence 14, Appl
9	54	98.2	502	10	US-09-903-068-18	Sequence 18, Appl
10	54	98.2	502	10	US-09-874-628-4	Sequence 4, Appli
11	54	98.2	532	9	US-09-982-543A-6	Sequence 6, Appli
12	54	98.2	532	9	US-10-153-217-2	Sequence 2, Appli
13	54	98.2	532	10	US-09-903-068-6	Sequence 6, Appli
14	54	98.2	532	10	US-09-903-068-14	Sequence 14, Appl
15	54	98.2	532	10	US-09-874-628-2	Sequence 2, Appli
16	52	94.5	493	10	US-09-742-684-12	Sequence 12, Appl
17	46	83.6	31	9	US-10-032-330-36	Sequence 36, Appl
18	46	83.6	505	10	US-09-771-161A-200	Sequence 200, App
19	46	83.6	505	10	US-09-903-068-8	Sequence 8, Appli
20	44	80.0	31	9	US-10-032-330-32	Sequence 32, Appl
21	44	80.0	503	10	US-09-903-068-10	Sequence 10, Appl
22	44	80.0	503	10	US-09-874-628-10	Sequence 10, Appl
23	43	78.2	505	10	US-09-903-068-16	Sequence 16, Appl
24	43	78.2	505	10	US-09-874-628-8	Sequence 8, Appli
25	41	74.5	673	10	US-09-874-198-8	Sequence 8, Appli
26	41	74.5	673	10	US-09-874-238-8	Sequence 8, Appli
27	41	74.5	760	10	US-09-925-301-1024	Sequence 1024, Ap
28	40	72.7	12	9	US-10-032-330-26	Sequence 26, Appl
29	40	72.7	12	10	US-09-736-076-26	Sequence 26, Appl
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31	38	69.1	124	10	US-09-939-980-529	Sequence 529, App
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35	36	65.5	11	9	US-10-032-330-10	Sequence 10, Appl
36	36	65.5	11	10	US-09-736-076-24	Sequence 24, Appl

37	36	65.5	11	10	US-09-736-076-66	Sequence 66, Appl
38	36	65.5	31	9	US-10-032-330-38	Sequence 38, Appl
39	36	65.5	198	10	US-09-925-302-500	Sequence 500, App
40	36	65.5	502	10	US-09-903-068-12	Sequence 12, Appl
41	36	65.5	503	9	US-09-982-543A-2	Sequence 2, Appli
42	36	65.5	503	9	US-10-005-228-4	Sequence 4, Appli
43	36	65.5	503	10	US-09-903-068-2	Sequence 2, Appli
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45	36	65.5	509	9	US-10-005-228-2	Sequence 2, Appli
46	36	65.5	509	10	US-09-903-068-4	Sequence 4, Appli
47	36	65.5	509	10	US-09-874-628-6	Sequence 6, Appli
48	35	63.6	11	10	US-09-736-076-23	Sequence 23, Appl
49	35	63.6	32	9	US-10-032-330-33	Sequence 33, Appl
50	35	63.6	513	10	US-09-742-684-2	Sequence 2, Appli
51	35	63.6	533	9	US-10-038-972A-15	Sequence 15, Appl
52	35	63.6	578	10	US-09-732-020-2	Sequence 2, Appli
53	35	63.6	598	9	US-10-038-972A-14	Sequence 14, Appl
54	35	63.6	735	9	US-10-038-972A-13	Sequence 13, Appl
55	35	63.6	735	9	US-10-293-478-1	Sequence 1, Appli
56	34	61.8	211	9	US-09-847-208-95	Sequence 95, Appl
57	34	61.8	321	9	US-09-847-208-73	Sequence 73, Appl
58	34	61.8	392	10	US-09-815-242-11795	Sequence 11795, A
59	34	61.8	1189	9	US-09-738-626-4140	Sequence 4140, Ap
60	34	61.8	1724	9	US-10-163-587A-17	Sequence 17, Appl
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63	33	60.0	502	9	US-10-028-072-548	Sequence 548, App
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77	33	60.0	502	9	US-10-143-114-548	Sequence 548, App
78	33	60.0	502	9	US-10-140-002-548	Sequence 548, App
79	33	60.0	502	9	US-09-746-783-148	Sequence 148, App
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83	33	60.0	502	9	US-10-036-150-40	Sequence 40, Appl
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85	33	60.0	502	9	US-10-142-423-548	Sequence 548, App
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92	33	60.0	502	9	US-10-140-921-548	Sequence 548, App
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100	33	60.0	502	9	US-10-160-498-548	Sequence 548, App

ALIGNMENTS

RESULT 1

US-10-032-330-21

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; Sequence 21, Application US/10032330
; Patent No. US20020165150A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel
; TITLE OF INVENTION: Tissue Remodeling
; FILE REFERENCE: BEN-SASSON=7
; CURRENT APPLICATION NUMBER: US/10/032,330
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/US00/32852
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: myristyl-G
US-10-032-330-21

Query Match 98.2%; Score 54; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GIVEEYQLPY 11

RESULT 3

US-09-736-076-25

; Sequence 25, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE
KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(11)
; OTHER INFORMATION: ALK3
US-09-736-076-25

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Best Local Similarity 100.0%; Pred. No. 0.00077;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

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Db 2 GIVEEYQLPY 11

RESULT 6

US-09-069-228-2

; Sequence 2, Application US/09069228

; Publication No. US20030073143A1

; GENERAL INFORMATION:

; APPLICANT: Gregory Plowman

; APPLICANT: Douglas Clary

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: Alk-7 RELATED DISORDERS

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSEQ for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/069,228

; FILING DATE: Filed herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/044,428

; FILING DATE: April 28, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/118

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-069-228-2

Query Match 98.2%; Score 54; DB 9; Length 493;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11
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Db 409 GIVEEYQLPY 418

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Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2003, 16:51:27 ; Search time 35 Seconds
(without alignments)
41.879 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
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3	54	98.2	11	23	AAU98367	Activin/TGFbR ALK3	
4	54	98.2	493	20	AAW89254	Human ALK-7. Homo	
5	54	98.2	496	22	AAE06222	Booroola sheep mut	
6	54	98.2	500	16	AAR74342	Truncated BRK-1.	
7	54	98.2	502	15	AAR55374	Mouse Activin rece	
8	54	98.2	502	16	AAR70238	Bone morphogenic p	
9	54	98.2	502	16	AAR85209	Mouse ALK-6. Mus	
10	54	98.2	502	17	AAR95226	Chick BMP type I r	
11	54	98.2	502	17	AAR96202	Bone morphogenetic	
12	54	98.2	502	20	AAV33307	Human mALK-6 clone	
13	54	98.2	502	20	AAW86249	Mouse BMP receptor	
14	54	98.2	502	22	AAE06221	Wild-type sheep BM	
15	54	98.2	502	22	AAE06225	Human BMP1B recept	
16	54	98.2	502	23	ABG61890	Prostate cancer-as	
17	54	98.2	532	15	AAR55368	Human Activin rece	
18	54	98.2	532	16	AAR74343	BRK-1 protein. Mu	
19	54	98.2	532	16	AAR70237	Bone morphogenic p	
20	54	98.2	532	16	AAR85207	Human ALK-3. Homo	
21	54	98.2	532	17	AAR95225	Mouse BMP type I r	
22	54	98.2	532	17	AAR96201	Bone morphogenetic	
23	54	98.2	532	20	AAV33301	Human hALK-3 clone	
24	54	98.2	532	20	AAV33305	Human mALK-3 from	
25	54	98.2	532	20	AAW86248	Mouse BMP receptor	
26	54	98.2	533	22	ABG22870	Novel human diagno	
27	54	98.2	564	22	ABG22876	Novel human diagno	

28	54	98.2	753	22	ABG22877	Novel human diagno
29	52	94.5	493	17	AAR95562	Serine threonine k
30	52	94.5	493	22	AAB47028	Rat activin recept
31	52	94.5	493	23	AAO14126	Protein of a rat-d
32	47	85.5	104	22	ABB11738	Human ALK-3 homolo
33	46	83.6	501	17	AAW03760	Mullerian inhibiti
34	46	83.6	505	14	AAR41921	MISR2A/MISR2B. Ra
35	46	83.6	505	15	AAR55369	Human Activin rece
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39	44	80.0	503	15	AAR55370	Human Activin rece
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44	43	78.2	505	16	AAR70240	Serine/threonine k
45	43	78.2	505	20	AAV33306	Human mALK-4 clone
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47	41	74.5	112	20	AAV27049	Amino acid sequenc
48	41	74.5	120	19	AAW38752	S. pneumoniae poss
49	41	74.5	760	21	AAB43579	Human cancer assoc
50	40	72.7	12	20	AAW74182	HJ loop peptide K0
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55	38	69.1	113	22	AAM38930	Human polypeptide
56	38	69.1	124	19	AAW77769	Staphylococcus aur
57	38	69.1	170	22	AAM40716	Human polypeptide
58	38	69.1	385	22	AAU34217	Staphylococcus aur
59	38	69.1	518	22	AAU36880	Staphylococcus aur
60	37	67.3	482	22	ABG05231	Novel human diagno
61	37	67.3	482	22	ABG29798	Novel human diagno
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63	36	65.5	11	23	AAU98324	Activin/TGFbR ALK1
64	36	65.5	11	23	AAU98366	Activin/TGFbR ALK1
65	36	65.5	198	21	AAB58162	Lung cancer associ
66	36	65.5	502	15	AAR55371	Mouse Activin rece
67	36	65.5	502	20	AAV33304	Human mALK-1 clone
68	36	65.5	503	15	AAR55366	Human Activin rece
69	36	65.5	503	16	AAR85210	Human ALK-1. Homo
70	36	65.5	503	17	AAR94602	TAR-3 polypeptide.
71	36	65.5	503	18	AAW27507	Human activin rece
72	36	65.5	503	20	AAV33299	Human hALK-1 clone

73	36	65.5	505	14	AAR41922	MISR3. Rattus rat
74	36	65.5	505	17	AAW03761	Mullerian inhibiti
75	36	65.5	509	14	AAR41920	MISR1. Rattus rat
76	36	65.5	509	15	AAR55367	Human Activin rece
77	36	65.5	509	16	AAR70239	Serine/threonine k
78	36	65.5	509	16	AAR85206	Human ALK-2. Homo
79	36	65.5	509	17	AAW03759	Mullerian inhibiti
80	36	65.5	509	17	AAR94601	TAR-1 polypeptide.
81	36	65.5	509	20	AAV33300	Human hALK-2 clone
82	36	65.5	584	20	AAV15222	Human receptor pro
83	36	65.5	584	22	AAB93398	Human protein sequ
84	36	65.5	1514	23	ABB92289	Herbicidally activ
85	35	63.6	11	20	AAW74179	HJ loop peptide K0
86	35	63.6	11	23	AAU98323	Activin/TGFbR ACTR
87	35	63.6	20	22	AAB50348	Adeno-associated v
88	35	63.6	130	22	ABG13497	Novel human diagno
89	35	63.6	138	21	AAG35116	Arabidopsis thalia
90	35	63.6	140	21	AAG35115	Arabidopsis thalia
91	35	63.6	145	23	ABP30567	Streptococcus poly
92	35	63.6	173	22	AAU49232	Propionibacterium
93	35	63.6	178	22	ABG13466	Novel human diagno
94	35	63.6	195	22	ABG25768	Novel human diagno
95	35	63.6	198	22	ABG10355	Novel human diagno
96	35	63.6	207	22	ABG21809	Novel human diagno
97	35	63.6	211	22	ABG24589	Novel human diagno
98	35	63.6	213	22	ABG17233	Novel human diagno
99	35	63.6	214	22	ABG24566	Novel human diagno
100	35	63.6	216	22	ABB62379	Drosophila melanog

ALIGNMENTS

RESULT 1

AAW74181

ID AAW74181 standard; peptide; 11 AA.

XX

AC AAW74181;

XX

DT 05-MAY-1999 (first entry)

XX

DE HJ loop peptide K098H101.

XX

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "myristylated"
FT Modified-site 11
FT /note= "amidated"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Disclosure; Fig 6; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which

CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX

SQ Sequence 11 AA;

Query Match 98.2%; Score 54; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

|||||||

Db 2 GIVEEYQLPY 11

RESULT 2

AAU98325

ID AAU98325 standard; Peptide; 11 AA.

XX

AC AAU98325;

XX

DT 13-AUG-2002 (first entry)

XX

DE Activin/TGFbR ALK3 serine-threonine kinase HJ loop peptide K098H101.

XX

KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;

KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

KW antiinflammatory; immunosuppressive; cardiant; haemostatic;

KW modulating STK activity; activin/TGFbR; ALK3; K098H101.

XX

OS Unidentified.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal myristyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN US2002049301-A1.

XX

PD 25-APR-2002.

XX

PF 13-DEC-2000; 2000US-0736076.

XX

PR 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX

PI Ben-Sasson SA;

XX

DR WPI; 2002-462787/49.

XX

PT New peptide from the HJ loop of serine-threonine kinase, useful for

PT treating e.g. cancer and for producing diagnostic antibodies -

XX

PS Disclosure; Fig 6; 41pp; English.

XX

CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the activin/TGFbR ALK3
CC serine-threonine kinase HJ loop peptide K098H101. This sequence is one
CC of the short peptides of the invention that selectively modulate the
CC activity of STK.

XX

SQ Sequence 11 AA;

Query Match 98.2%; Score 54; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11

|||||||

Db 2 GIVEEYQLPY 11

Search completed: June 25, 2003, 16:58:45

Job time : 37 secs

OM protein - protein search, using sw model

Run on: June 25, 2003, 16:58:07 ; Search time 26 Seconds
(without alignments)
12.448 Million cell updates/sec

Title: US-10-032-330-21
Perfect score: 55
Sequence: 1 XGIVEEYQLPY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	%					
Result		Query				
No.	Score	Match	Length	DB	ID	Description

1	54	98.2	500	4	US-08-158-735A-2	Sequence 2, Appli
2	54	98.2	502	2	US-08-481-337A-8	Sequence 8, Appli
3	54	98.2	502	4	US-09-382-256-18	Sequence 18, Appl
4	54	98.2	502	4	US-09-395-115-18	Sequence 18, Appl
5	54	98.2	502	4	US-08-123-934A-4	Sequence 4, Appli
6	54	98.2	502	4	US-08-334-179A-14	Sequence 14, Appl
7	54	98.2	502	4	US-08-436-265-18	Sequence 18, Appl
8	54	98.2	502	4	US-09-679-187-18	Sequence 18, Appl
9	54	98.2	502	5	PCT-US94-10080-4	Sequence 4, Appli
10	54	98.2	502	5	PCT-US95-05467-8	Sequence 8, Appli
11	54	98.2	532	2	US-08-481-337A-6	Sequence 6, Appli
12	54	98.2	532	4	US-09-382-256-6	Sequence 6, Appli
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29	52	94.5	493	2	US-08-957-364-2	Sequence 2, Appli
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34	46	83.6	505	4	US-09-382-256-8	Sequence 8, Appli
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65	36	65.5	503	4	US-08-436-265-2	Sequence 2, Appli
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68	36	65.5	503	5	PCT-US95-05467-2	Sequence 2, Appli
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72	36	65.5	509	1	US-08-317-847-14	Sequence 14, Appl
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74	36	65.5	509	4	US-09-382-256-4	Sequence 4, Appli
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84	35	63.6	513	2	US-08-459-009-10	Sequence 10, Appl
85	35	63.6	513	2	US-08-459-009-11	Sequence 11, Appl
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87	35	63.6	513	3	US-08-459-951-10	Sequence 10, Appl
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93	35	63.6	536	2	US-08-357-533A-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1

US-08-158-735A-2

; Sequence 2, Application US/08158735A

; Patent No. 6248554

; GENERAL INFORMATION:

; APPLICANT: COOK, JONATHAN S.

; APPLICANT: CORREA, PAUL E.

; APPLICANT: KOENIG, BETH B.

; APPLICANT: ROSENBAUM, JAN S.

; APPLICANT: TING, JERRY

; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THE PROCTER & GAMBLE COMPANY

; STREET: 11810 EAST MIAMI RIVER ROAD

; CITY: ROSS

; STATE: OH

; COUNTRY: USA

; ZIP: 45061

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/158,735A

; FILING DATE: 24-NOV-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-158-735A-2

Query Match 98.2%; Score 54; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIVEEYQLPY 11
|||||||
Db 448 GIVEEYQLPY 457

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